FULL LENGTH APO-A1 SEQUENCE

1
MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVD

VLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKE

TEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHE
194
LQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHA
267
KATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNTQ (SEQ ID NO:2)

sig_peptide 20..91
mature_protein 92..820

20 a tgaaagctgc ggtgctgacc ttggccgtgc tcttcctgac

61 ggggagccag gctcggcatt tctggcagca agatgaaccc ccccagagcc cctgggatcg

121 agtgaaggac ctggccactg tgtacgtgga tgtgctcaaa gacagcggca gagactatgt

181 gtcccagttt gaaggctccg ccttgggaaa acagctaaac ctaaagctcc ttgacaactg

241 ggacagcgtg acctccacct tcagcaagct gcgcgaacag ctcggccctg tgacccagga

301 gttctgggat aacctggaaa aggagacaga gggcctgagg caggagatga gcaaggatct

361 ggaggaggtg aaggccaagg tgcagcccta cctggacgac ttccagaaga agtggcagga

421 ggagatggag ctctaccgcc agaaggtgga gccgctgcgc gcagagctcc aagagggcgc

481 gcgccagaag ctgcacgagc tgcaagagaa gctgagccca ctgggcgagg agatgcgcga

541 ccgcgcgcgc gcccatgtgg acgcgctgcg cacgcatctg gccccctaca gcgacgagct

601 gcgccagcgc ttggccgcgc gccttgaggc tctcaaggag aacggcggcg ccagactggc

661 cgagtaccac gccaaggcca ccgagcatct gagcacgctc agcgagaagg ccaagcccgc

721 gctcgaggac ctccgccaag gcctgctgcc cgtgctggag agcttcaagg tcagcttcct

781 gagcgctctc gaggagtaca ctaagaagct caacacccag (SEQ ID NO:1)

FIG. 1A

18K N-TERMINAL FRAGMENT

25
DEPPQSPWDRVKDLATVYVD

VLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKE

TEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHE

194
LQEKLSPLGEEMRDRARAHVDALRTHLAPYSDEL (SEQ ID NO:3)

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 92  gatgaaccc ccccagagcc cctgggatcg

121 agtgaaggac ctggccactg tgtacgtgga tgtgctcaaa gacagcggca gagactatgt

181 gtcccagttt gaaggctccg ccttgggaaa acagctaaac ctaaagctcc ttgacaactg

241 ggacagcgtg acctccacct tcagcaagct gcgcgaacag ctcggccctg tgacccagga

301 gttctgggat aacctggaaa aggagacaga gggcctgagg caggagatga gcaaggatct

361 ggaggaggtg aaggccaagg tgcagcccta cctggacgac ttccagaaga agtggcagga

421 ggagatggag ctctaccgcc agaaggtgga gccgctgcgc gcagagctcc aagagggcgc

481 gcgccagaag ctgcacgagc tgcaagagaa gctgagccca ctgggcgagg agatgcgcga

541 ccgcgcgcgc gcccatgtgg acgcgctgcg cacgcatctg gccccctaca gcgacgagct

601 g (SEQ ID NO:4)
```

FIG. 1B

13K N-TERMINAL FRAGMENT

25
DEPPQSPWDRVKDLATVYVD

VLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKE

144
TEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVE (PORTION OF SEQ ID NO:3)

```
 92  gatgaaccc ccccagagcc cctgggatcg

121 agtgaaggac ctggccactg tgtacgtgga tgtgctcaaa gacagcggca gagactatgt

181 gtcccagttt gaaggctccg ccttgggaaa acagctaaac ctaaagctcc ttgacaactg

241 ggacagcgtg acctccacct tcagcaagct gcgcgaacag ctcggccctg tgacccagga

301 gttctgggat aacctggaaa aggagacaga gggcctgagg caggagatga gcaaggatct

361 ggaggaggtg aaggccaagg tgcagcccta cctggacgac ttccagaaga agtggcagga

421 ggagatggag ctctaccgcc agaaggtgga g (PORTION OF SEQ ID NO:4)
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FIG. 1C

13K C-TERMINAL FRAGMENT

156
QKLHE

194
LQEKLSPLGEEMRD RARAHVDALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHA

267
KATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNTQ (PORTION OF SEQ ID NO:2)

485 cagaag ctgcacgagc tgcaagagaa gctgagccca ctgggcgagg agatgcgcga

541 ccgcgcgcgc gcccatgtgg acgcgctgcg cacgcatctg gccccctaca gcgacgagct

601 gcgccagcgc ttggccgcgc gccttgaggc tctcaaggag aacggcggcg ccagactggc

661 cgagtaccac gccaaggcca ccgagcatct gagcacgctc agcgagaagg ccaagcccgc

721 gctcgaggac ctccgccaag gcctgctgcc cgtgctggag agcttcaagg tcagcttcct

781 gagcgctctc gaggagtaca ctaagaagct caacacccag (PORTION OF SEQ ID NO:1)

FIG. 1D